RESISTANCE TO *Cowpea mild mottle virus* IN THE EMBRAPA CARIOCA SEEDED COMMON BEAN CULTIVAR BRS SUBLIME

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INTRODUCTION

In Brazil, the *Cowpea mild mottle virus* (CPMMV) was firstly reported in common bean in 1980, in Campinas, São Paulo (Costa *et al*., 1983). The most common symptoms are a mild mosaic along or between the leaf veins and leaf crinckling. In susceptible soybean genotypes, strong stem necrosis is also observed. The symptoms of CPMMV was clearly identified in common bean fields grown with the cultivar BRS FC401 RMD that presents effective resistance to *Bean golden mosaic virus* (BGMV) (event Embrapa 5.1), but it is susceptible to CPMMV (Souza *et al*., 2018). Both viruses are transmitted by the whitefly (*Bemisia tabaci*). Sources of resistance to CPMMV have been identified through greenhouse and field screenings carried out at Embrapa Arroz e Feijão. The main goal of the present work was to elucidate the genetic inheritance of the CPMMV resistance present in BRS Sublime, an Embrapa cultivar with carioca seed type identified as the most promising CPMMV resistance source in Brazil so far.

MATERIALS AND METHODS

Controlled crosses were carried out at Embrapa Arroz e Feijão between the resistance source, BRS Sublime, and the transgenic line CNFCT 16207 (event Embrapa 5.1), susceptible to CPMMV. CNFCT 16207 was always used as the male parent. All F_1 plants were tested with event-specific molecular markers for transgene presence identification to confirm them as hybrids. The checked hybrids were advanced up to generations F_2 and $F_{2:3}$. All plants were maintained in an insect-proof net house. A total of 180 F_2 individual plants and 180 $F_{2:3}$ progenies (2,160 seedlings; 12 seedlings/progeny), in addition to the parents, were mechanical inoculation with a CPMMV isolate (strain CPMMV:BR:GO:14 – GenBank MK202583) at 8 days after planting, according to Alves-Freitas *et al*. (2019). For inoculation, leaves from the transgenic BGMV-resistant common bean line CNFCT 16207, showing severe symptoms of crinkling, were ground in 0.1 M phosphate buffer with 0.1% sodium sulfite, and was applied using carborundum 500 mesh. The inoculum was rubbed on the first trifoliate leaf (Cheruku *et al*., 2017). Four-to-five weeks after inoculation, all plants were scored for CPMMV severity. The scoring scale used to evaluate virus severity ranged from 1 (absence of disease symptoms and signs of pathogens) to 9 (80-100% disease severity or plant death) (Melo, 2009). Plants showing scores of 1-to-3 were considered resistant, and those scoring 4 or higher were considered susceptible. Chi-square (χ^2) tests ($p \leq 0.05$) were performed for goodness of fit to test the deviation of the observed segregation data from the theoretically expected Mendelian segregation ratio.

RESULTS AND DISCUSSION

All tested plants of BRS Sublime were resistant to the isolate CPMMV:BR:GO:14 and all plants of CNFCT 16207 were susceptible. From the 180 F_2 individual plants evaluated, 128 plants showed resistant reactions and 52 were susceptible. The segregation for resistance to CPMMV in the F_2 population showed a goodness of fit of 3 resistant: 1 susceptible (3R: 1S; $\chi^2 = 1.45$, P = 22.8%). Regarding the 180 $F_{2:3}$ progenies tested for CPMMV reaction, 45 shown non-segregating resistance, 88 progenies segregated for CPMMV reaction, and the other 47 progenies shown non-segregating susceptibility (1RR: 2Rr: 1Rr; $\chi^2 = 0.13$, P = 93.5%). Results from both generations indicated that a single dominant gene controls the inheritance of CPMMV resistance in common bean cultivar BRS Sublime. This is the first report of a genetic inheritance study for CPMMV resistance in common bean. The populations used in the present work are being genotyped with SNP markers to genetically map the CPMMV resistance locus present in BRS Sublime.

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